

## Supplementary Materials:

**Table S1.** Code of Isolates.

<b>Mycorrhizal isolate</b>	<b>Isolation year</b>	<b>Isolate ID</b>
<i>Claroideoglomus claroideum</i>	2014	87-5C
<i>Claroideoglomus lamellosum</i>	2017	57-4G
<i>Glomus</i> species	2017	69-6A
<i>Racocetra fulgida</i>	2017	57-4G

**Table S2.** Biomass explained by CO<sub>2</sub>, mycorrhizae, species, and growth chamber. Significant codes are for alpha thresholds.

### S2: Analysis of Variance (ANOVA)

#### Source of biomass variation

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
CO <sub>2</sub>	1	52.08	52.08	8.5256	0.00407	**
Mycorrhizae	1	1436.55	1436.55	235.1612	< 2.2e-16	***
Species	5	547.96	109.59	17.9400	8.768e-14	***
Chamber	1	2.02	2.02	0.3302	0.56643	
CO <sub>2</sub> :Mycorrhizae	1	34.76	34.76	5.6905	0.01837	*
CO <sub>2</sub> :Species	5	77.62	15.52	2.5412	0.03091	*
Mycorrhizae:Species	5	483.63	96.73	15.8339	2.146e-12	***
CO <sub>2</sub> :Chamber	1	0.51	0.51	0.0834	0.77311	
Mycorrhizae:Chamber	1	3.14	3.14	0.5142	0.47450	
Species:Chamber	5	50.86	10.17	1.6652	0.14675	
CO <sub>2</sub> :Mycorrhizae:Species	5	60.78	12.16	1.9899	0.08361	.
CO <sub>2</sub> :Mycorrhizae:Chamber	1	0.01	0.01	0.0014	0.97003	
CO <sub>2</sub> :Species:Chamber	5	13.72	2.74	0.4492	0.81329	
Mycorrhizae:Species:Chamber	5	62.58	12.52	2.0487	0.07535	.
CO <sub>2</sub> :Mycorrhizae:Species:Chamber	5	11.95	2.39	0.3911	0.85427	
Residuals	143	873.56	6.11			
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Signif. codes:	0	****	0.001	***	0.01	**
				0.05	.	.
				0.1		1

**Table S3.** Root morph. explained by CO2, mycorrhizae, species and growth chamber. Significant codes are for alpha thresholds

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**S3: Analysis of Variance (ANOVA)**

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**Source of relative transportive root variation**

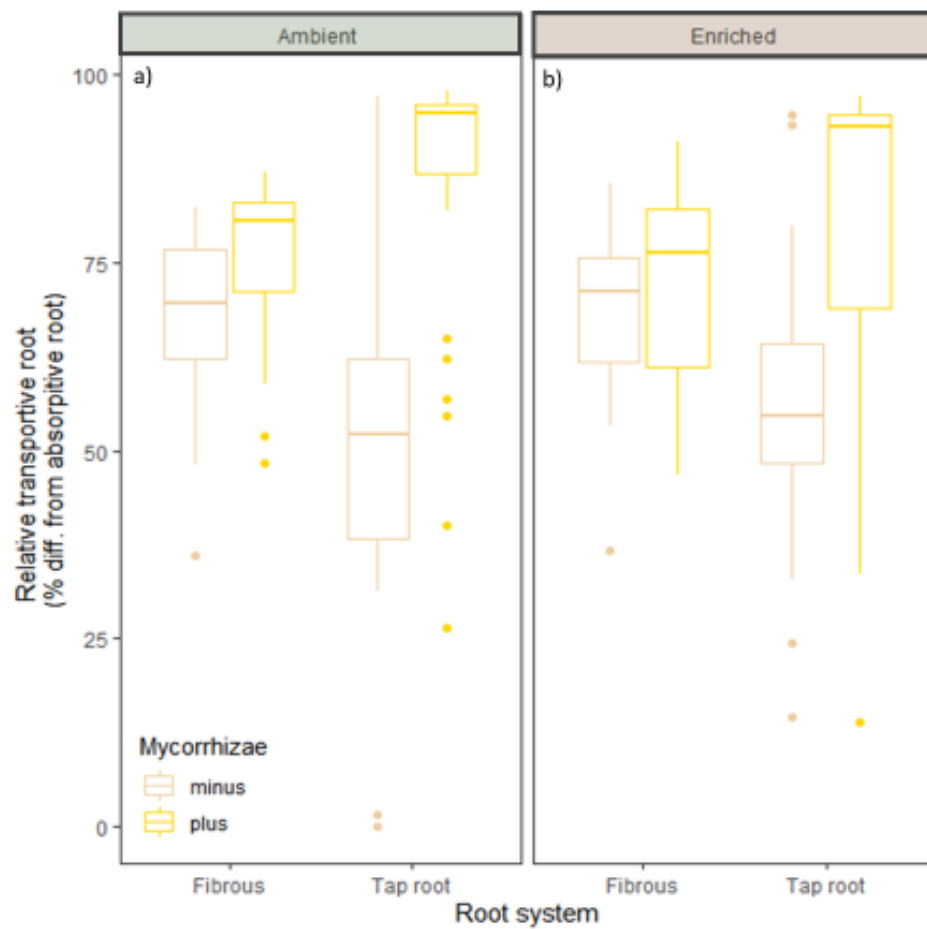
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	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
CO2	1	56	55.5	0.2289	0.63305	
Mycorrhizae	1	22277	22277.1	91.8808	< 2.2e-16	***
Species	5	10834	2166.9	8.9373	2.083e-07	***
Chamber	1	286	285.8	1.1786	0.27947	
CO2:Mycorrhizae	1	1111	1110.6	4.5807	0.03403	*
CO2:Species	5	1187	237.4	0.9791	0.43275	
Mycorrhizae:Species	5	11550	2309.9	9.5271	7.317e-08	***
CO2:Chamber	1	75	74.9	0.3090	0.57919	
Mycorrhizae:Chamber	1	638	638.3	2.6328	0.10688	
Species:Chamber	5	1275	255.0	1.0519	0.38978	
CO2:Mycorrhizae:Species	5	804	160.7	0.6629	0.65219	
CO2:Mycorrhizae:Chamber	1	108	108.5	0.4473	0.50469	
CO2:Species:Chamber	5	1613	322.6	1.3304	0.25465	
Mycorrhizae:Species:Chamber	5	304	60.8	0.2507	0.93889	
CO2:Mycorrhizae:Species:Chamber	5	639	127.8	0.5273	0.75531	
Residuals	143	34671	242.5			
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Signif. codes:	0	'***'	0.001	'**'	0.01	'*'
				0.05	'.'	0.1
						' ' 1

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**Figure S1.** The effect of CO<sub>2</sub> and mycorrhizae on fibrous root systems. Irrespective of CO<sub>2</sub> regime, +mycorrhizae yielded a larger effect on tap-root systems.

**Table S4.** GenBank Accession table. Below Are the Corresponding Accessions Used to Construct the Phylogenetic Tree for the 6 *Asclepias* spp.

<b><i>Asclepias rbcl</i> Accessions</b>		
<i>A. incarnata</i>	[protein = ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = QBP44096.1]	Accession: MK525246.1 [gene = rbcl]
<i>A. sullivantii</i>	[protein = ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = QBP44100.1]	Accession: MK525250.1 [gene = rbcl]
<i>A. syriaca</i>	[protein = ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = AEH27042.1]	Accession: HQ384906.1 [gene = rbcl]
<i>A. tuberosa</i>	[protein = ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = QGV12460.1]	Accession: MN601492.1 [gene = rbcl]
<i>A. verticillata</i>	[protein = ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = AKG48691.1]	Accession: KJ773290.1 [gene = rbcl]
<i>A. viridis</i>	[protein = ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit] [protein_id = QCW23980.1]	Accession: MH549741.1 [gene = rbcl]